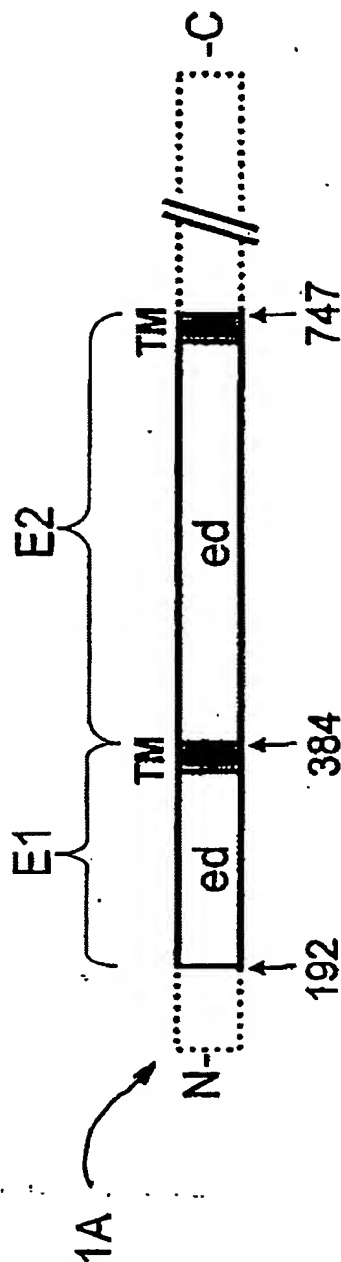


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TME1: 347-MIAGAHWGVLGIA^UYFSMVGNWAKVLVLLLFAGVDA-383

*** * * * * ** ***** * *

TME2: 717-EYVLLFLLLADARVCCLWMLLISQAEA-746

***** * * ***** * *

FIG. 1

[illegible]

U

5' _GGGAATGCCATATGATCGTGGTG_3'
5'_ATGCCATATGATCGCTGGTGCTCAGTGGGGTGTTCTGGCTGGTATCGCTTACTTCTCTATGGTTGGTAAC..
3'_TACGGTATAC TAGCGACCAACGAGTGACCCCCACAAGACCGACCATAGCGGAATGAAGAGATACCAACCATG..
Clal
...TGGGCTAAAGCTTCTGGTTGTTCTGCTGCTGTTCTGCTGGTGTGACGCTTAGATCGATATGC_3' 131 bases
...ACCCGATTTC AAGACCAACAAGACGACGACCAAGCGACCAACTGCCGAATCTAGCTATACG_5'
3'_ACAACTGGGAATCTAGCTATACG_5'

FIG. 2

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D

OL11(+): 5'atgccatgatcgctgctcactggggtgtctggctggtatcgcttacttctctatggttgtaactggg
OL12(-): 5'gcataatcgatctaagcgtaacaccagcgacagcagcagagaaccagaactttagccagttaccaaccatagagaa

Cloning in pT7-7:

OL13(+): 5'gggaatgccatgatcgctgggtg
OL14(-): 5'gcataatcgatctaagcgtaacaa

Cloning in pGEXKT:

OL15(+): 5'ggatccatggaatacgtgttc (without DP site)
OL17(+): 5'ggatccgaacccgatggaatacgtgttc (with DP site)
OL16(-): 5'gaattcctaagcttcagcctgag

Cloning in pET32a:

OL18(+): 5'gtgatatctgatctgtggtggtgt (hybridizes to the segment 915-932 of pGEXKT)
OL16(-): 5'gaattcctaagccttcagcctgag

Cloning in pT7-7 of (M)DP-TME1::

OL19 (+) : 5'- CGCATATGGACCCGATCGCTGGTGCT -3' (Nde I underlined)
OL20 (-) : 5'-GAATTCCTAAGCGTCAACACCAGC-3' (EcoR I underlined)

FIG. 2

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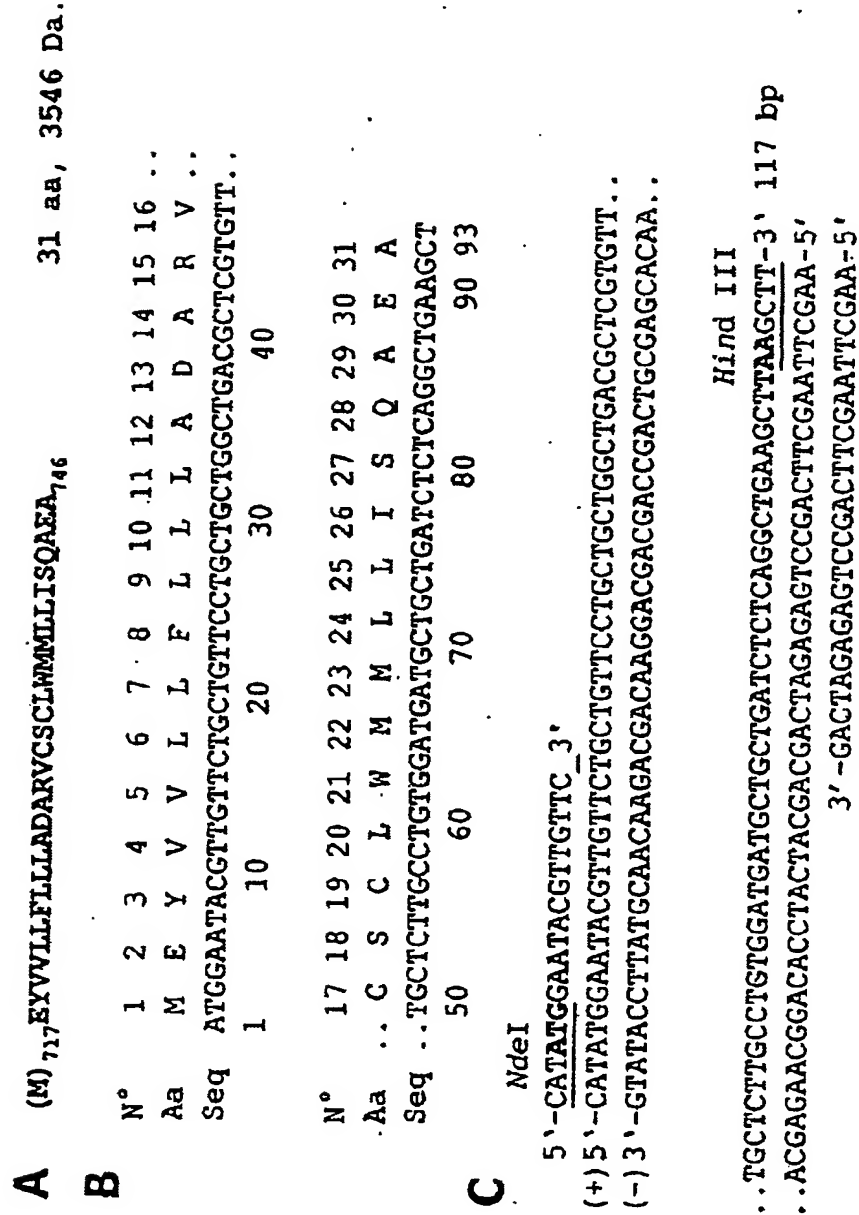


FIG. 3

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D

OL21(+): 5'catatgaatacgttgttctgctgttctgctgctgctgctgacgctcgtgttgctcttgccctgtggat
OL22(-): 5'aagcttaagcttcagcctgagagatcagcagcatcatccacaggcaagagcaaacac

Cloning in pT7-7:

OL23(+): 5'catatgaatacgttggttc
OL24(-): 5'aagcttaagcttcagcctgagagatcag

Cloning in pGEXKT:

OL25(+): 5'ggatccgaatacgttggttc (without DP site)
OL27(+): 5'ggatccgacccgggaatacgttggttc (with DP site)
OL26(-): 5'gaattcttaagcttcagcctgagagatcag

Cloning in pET32a:

OL18(+): 5'gtgatatctgatctgtctgtggtggt (hybridizes to the segment 915-932 of pGEXKT)
OL26(-): 5'gaattcttaagcttcagcctgagagatcag

Cloning in pT7-7 of (M)DP-TME2:

OL28 (+) : 5'- CGCATATATGACCCGGAATACGTTGTTC-3' (Nde I underlined)
OL29 (-) : 5'-CAGAATTCCTAAGCTTCAGCCTGAGAG-3' (EcoR I underlined)

FIG. 3

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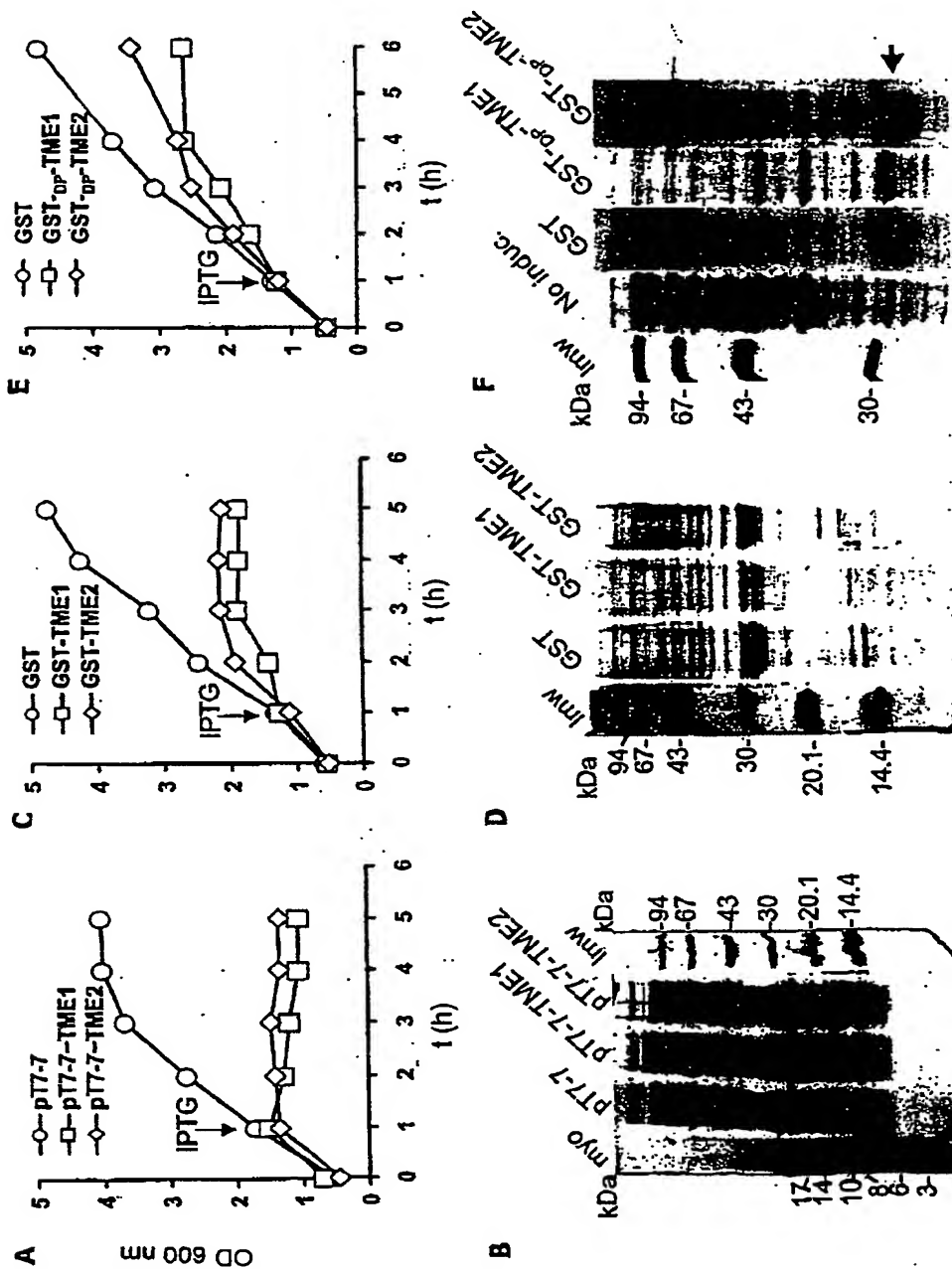


FIG. 4

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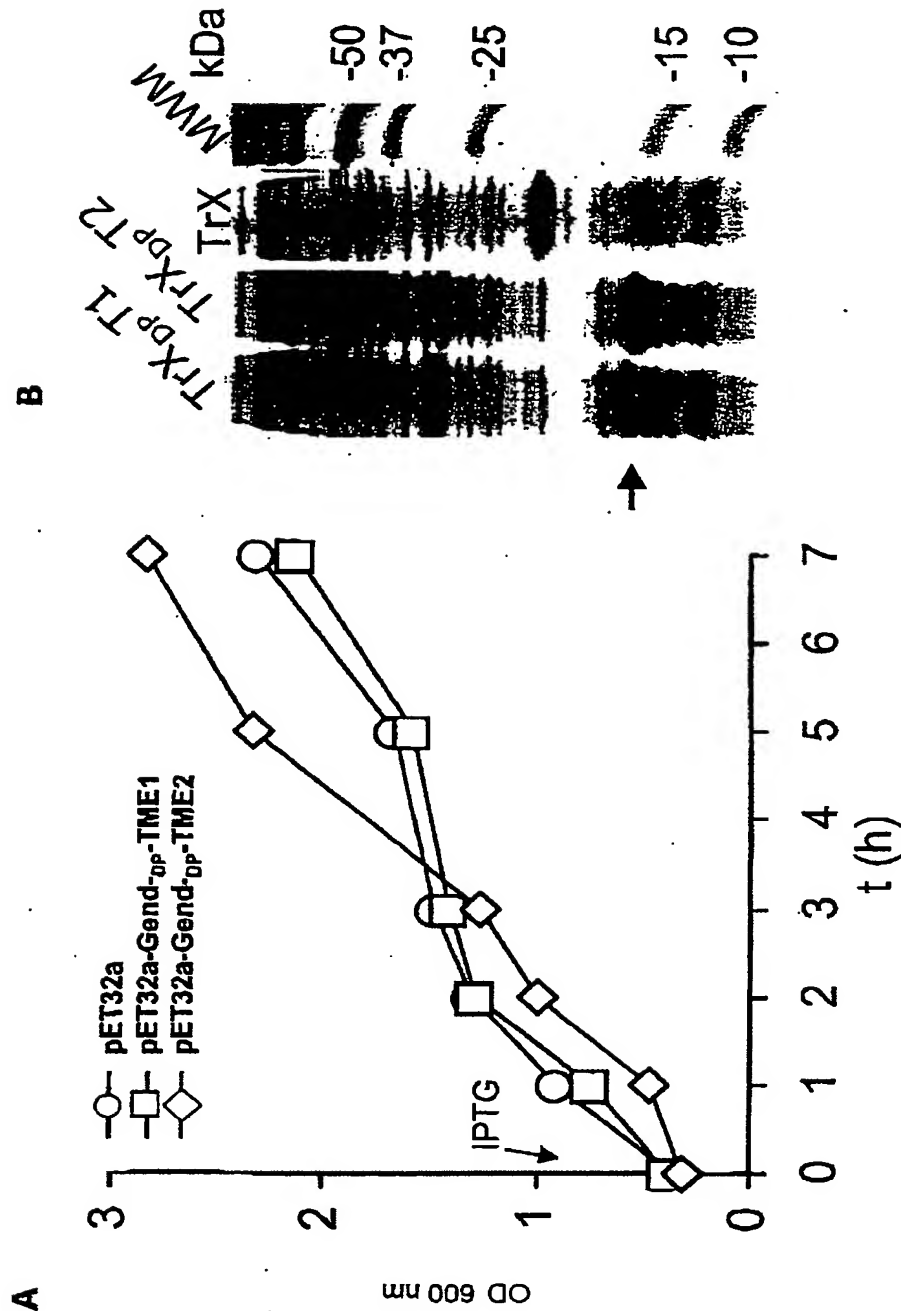


FIG. 5

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GST :
 MSPILGYWKIKGLVQPTRLLEYLEEKYEHL YERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIRIYA
 ADKHNMLGGCPKERAESIMLEGAVLDIRYGVSR IAYSKDFETLVDFLSKLPMLKMFEDRLCHKTYLNGDHVTH
 PDEWLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWAATFGGSDHPPKSDLSGGG
GGLVPRGS/PGIHRD

GST-TME2 :
 MSPILGYWKIKGLVQPTRLLEYLEEKYEHL YERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIRIYA
 DKHNMLGGCPKERAESIMLEGAVLDIRYGVSR IAYSKDFETLVDFLSKLPMLKMFEDRLCHKTYLNGDHVTHPD
 FMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWAATFGGSDHPPKSDLSGGGGL
VPRGS/EYVLLFIILADARVCCLWMLLISQAEA

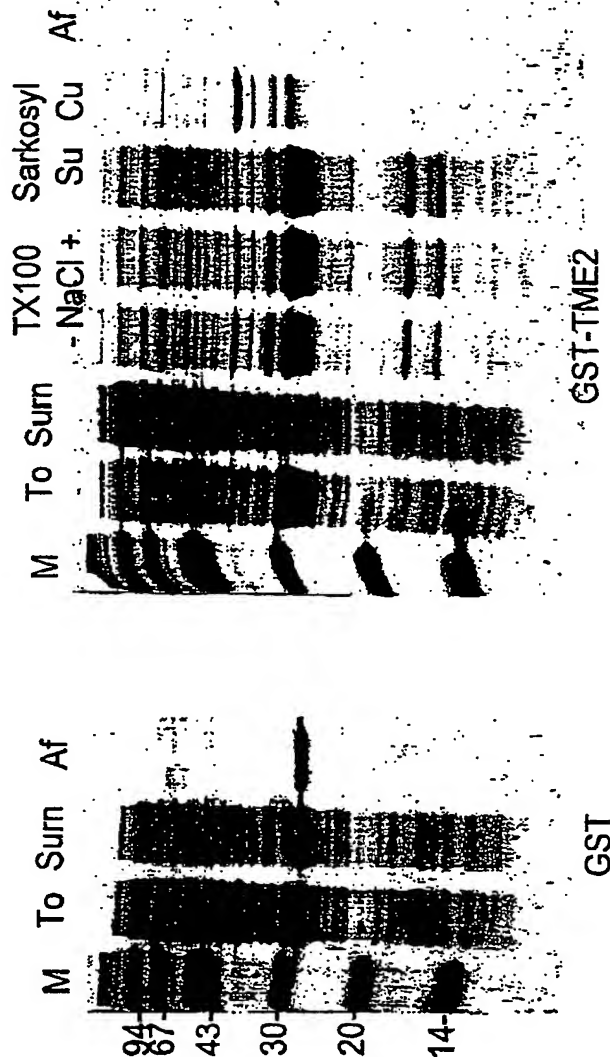


FIG. 6

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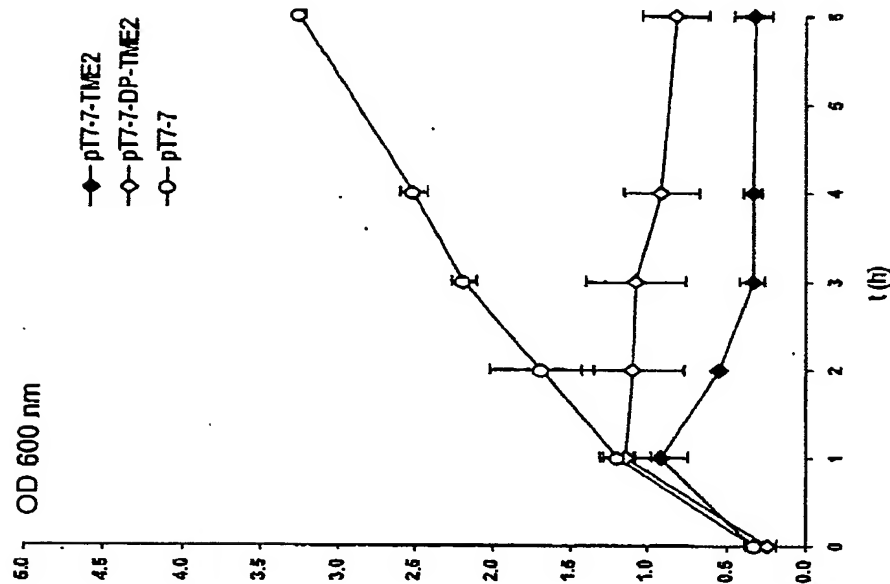


FIG. 7B

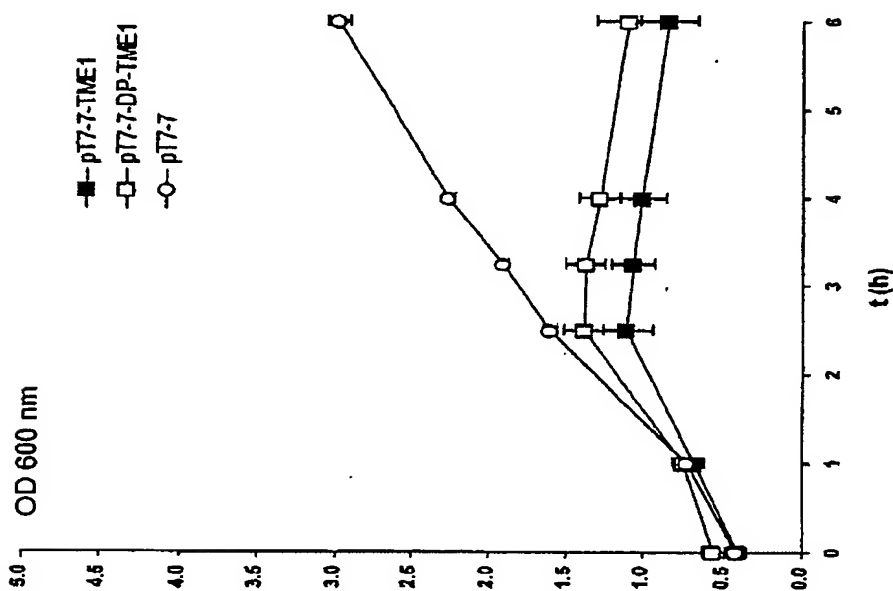


FIG. 7A